Listing of Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-10. (Cancelled).

11. (Previously presented) A method for screening a collection of compounds to determine those compounds which bind to receptors of the activin/TGF-β superfamily, said method comprising employing a vertebrate activin receptor in a competitive binding assay,

wherein said vertebrate activin receptor is encoded by a nucleotide sequence which is:

(a) the nucleotide sequence of a cDNA molecule present in a vertebrate library, wherein the noncoding strand of the cDNA molecule hybridizes under conditions of low stringency with a probe comprising the contiguous sequence of nucleotides 128-1609 of SEQ ID NO:15; or

(b) a sequence degenerate with the sequence of a cDNA molecule according to (a);

wherein the receptor is further characterized by having the following domains, reading from the N-terminal end of said protein:

an extracellular, ligand-binding domain,

a hydrophobic, trans-membrane domain, and

an intracellular serine/threonine kinase domain.

12-17. (Cancelled).

18. (Previously presented) A method according to claim 11, wherein said receptor is encoded by nucleotides having at least 70% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-1609 of SEQ ID NO:15.

19. (Previously presented) A method according to claim 11, wherein said receptor is encoded by nucleotides having at least 80% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-1609 of SEQ ID NO:15.

20. (Previously presented) A method according to claim 11, wherein said receptor is encoded by nucleotides having at least 90% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-1609 of SEQ ID NO:15.

21. (Previously presented) A method according to claim 11, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

22. (Previously presented) A method according to claim 18, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

23. (Previously presented) A method according to claim 19, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

24. (Previously presented) A method according to claim 20, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

25. (Previously presented) A method according to claim 11, wherein said receptor comprises the amino acid sequence of residues 20-513 as set forth in SEQ ID NO:16.

26. (Previously presented) A method according to claim 25, wherein said receptor further comprises the amino acid sequence of residues 1-19 as set forth in SEQ ID NO:16.

27. (Previously presented) A method for screening a collection of compounds to determine those compounds which bind to receptors of the activin/TGF-β superfamily, said method comprising employing a soluble polypeptide in a competitive binding assay,

wherein said soluble polypeptide is encoded by a nucleotide sequence which is:

(a) the nucleotide sequence of a cDNA molecule present in a vertebrate library, wherein the noncoding strand of the cDNA molecule hybridizes under conditions of low stringency with a probe comprising the contiguous sequence of nucleotides 128-472 of SEQ ID NO: 15; or

(b) a sequence degenerate with the sequence of a cDNA molecule according to (a).

28. (Previously presented) A method according to claim 27, wherein said polypeptide is encoded by nucleotides having at least 70% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-472 of SEQ ID NO:15.

29. (Previously presented) A method according to claim 27, wherein said receptor is encoded by nucleotides having at least 80% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-472 of SEQ ID NO:15.

30. (Previously presented) A method according to claim 27, wherein said receptor is encoded by nucleotides having at least 90% sequence identity with respect to the contiguous nucleotide sequence of nucleotides 128-472 of SEQ ID NO:15.

31. (Previously presented) A method according to claim 27, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

32. (Previously presented) A method according to claim 28, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

33. (Previously presented) A method according to claim 29, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

34. (Previously presented) A method according to claim 30, wherein the contiguous nucleotide sequence further comprises nucleotides 71-127 of SEQ ID NO:15.

35. (Previously presented) A method according to claim 27, wherein said receptor comprises the amino acid sequence of residues 20-134 as set forth in SEQ ID NO:16.

36. (Previously presented) A method according to claim 35, wherein said receptor further comprises the amino acid sequence of residues 1-19 as set forth in SEQ ID NO:16.